RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: *10/758,636*

Source: *1FWO*

Date Processed by STIC: *1/27/04*

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221
Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , **EFS Submission User Manual** - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 4B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

Raw Sequence Listing Error Summary

| ERROR DETECTED | SUGGESTED CORRECTION | SERIAL NUMBER: 10/758,636 |

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____ Wrapped Nucleics — The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
_____ Wrapped Aminos — was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will
prevent "wrapping."

2 ____ Invalid Line Length — The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ____ Misaligned Amino — The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers;
_____ Numbering — use space characters, instead.

4 ____ Non-ASCII — The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please
ensure your subsequent submission is saved in ASCII text.

5 ____ •Variable Length — Sequence(s) ___ contain n's or Xaa's representing more than one residue. Per Sequence Rules,
each n or Xaa can only represent a single residue. Please present the maximum number of each
residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ____ PatentIn 2.0 — A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
_____ "bug" — sequences(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for
Artificial or Unknown sequences.

7 ____ Skipped Sequences — Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
_____ (OLD RULES) — (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 ____ Skipped Sequences — Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
_____ (NEW RULES) — <210> sequence id number
<400> sequence id number
000

9 ____ Use of n's or Xaa's — Use of n's and/or Xaa's have been detected in the Sequence Listing.
_____ (NEW RULES) — Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 ____ Invalid <213> — Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
_____ Response — scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or
is Artificial Sequence

11 ____ Use of <220> — Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
"Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 07/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12 ____ PatentIn 2.0 — Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
_____ "bug" — resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ____ Misuse of n/Xaa — "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid

AMC – Biotechnology Systems Branch – 09/09/2003

IFWO

RAW SEQUENCE LISTING
PATENT APPLICATION: **US/10/758,636**

DATE: 01/27/2004
TIME: 10:59:30

Input Set : **A:\35966C.txt**
Output Set: **N:\CRF4\01272004\J758636.raw**

```
    4 <110> APPLICANT: Han, Hui-Quan
    5        Kwak, Keith
    7 <120> TITLE OF INVENTION: Human E3 Alpha Ubiquitin Ligase Family
    9 <130> FILE REFERENCE: 01017/35966C
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/758,636
C--> 12 <141> CURRENT FILING DATE: 2003-01-15
   14 <150> PRIOR APPLICATION NUMBER: US 09/724,126
   15 <151> PRIOR FILING DATE: 2000-11-28
   17 <150> PRIOR APPLICATION NUMBER: US 60/187,911
   18 <151> PRIOR FILING DATE: 1999-03-08
   20 <160> NUMBER OF SEQ ID NOS: 29
   22 <170> SOFTWARE: PatentIn Ver. 2.0
```

Does Not Comply
Corrected Diskette Needed

ERRORED SEQUENCES

```
  511 <210> SEQ ID NO: 2
  512 <211> LENGTH: 1749
  513 <212> TYPE: PRT
  514 <213> ORGANISM: Homo sapiens
  516 <400> SEQUENCE: 2
  517 Met Ala Asp Glu Glu Ala Gly Gly Thr Glu Arg Met Glu Ile Ser Ala
  518   1               5                  10                  15
  520 Glu Leu Pro Gln Thr Pro Gln Arg Leu Ala Ser Trp Trp Asp Gln Gln
  521             20                  25                  30
  523 Val Asp Phe Tyr Thr Ala Phe Leu His His Leu Ala Gln Leu Val Pro
  524         35                  40                  45
  526 Glu Ile Tyr Phe Ala Glu Met Asp Pro Asp Leu Glu Lys Gln Glu Glu
  527       50                  55                  60
  529 Ser Val Gln Met Ser Ile Phe Thr Pro Leu Glu Trp Tyr Leu Phe Gly
  530   65                  70                  75                  80
  532 Glu Asp Pro Asp Ile Cys Leu Glu Lys Leu Lys His Ser Gly Ala Phe
  533                 85                  90                  95
  535 Gln Leu Cys Gly Arg Val Phe Lys Ser Gly Glu Thr Thr Tyr Ser Cys
  536             100                 105                 110
  538 Arg Asp Cys Ala Ile Asp Pro Thr Cys Val Leu Cys Met Asp Cys Phe
  539             115                 120                 125
  541 Gln Asp Ser Val His Lys Asn His Arg Tyr Lys Met His Thr Ser Thr
  542         130                 135                 140
  544 Gly Gly Gly Phe Cys Asp Cys Gly Asp Thr Glu Ala Trp Lys Thr Gly
  545 145                 150                 155                 160
  547 Pro Phe Cys Val Asn His Glu Pro Gly Arg Ala Gly Thr Ile Lys Glu
  548                 165                 170                 175
```

RAW SEQUENCE LISTING   DATE: 01/27/2004
PATENT APPLICATION: US/10/758,636   TIME: 10:59:30

Input Set : A:\35966C.txt
Output Set: N:\CRF4\01272004\J758636.raw

```
550 Asn Ser Arg Cys Pro Leu Asn Glu Glu Val Ile Val Gln Ala Arg Lys
551             180             185                 190
553 Ile Phe Pro Ser Val Ile Lys Tyr Val Val Glu Met Thr Ile Trp Glu
554             195             200                 205
556 Glu Glu Lys Glu Leu Pro Pro Glu Leu Gln Ile Arg Glu Lys Asn Glu
557     210             215                 220
559 Arg Tyr Tyr Cys Val Leu Phe Asn Asp Glu His His Ser Tyr Asp His
560 225             230                 235                 240
562 Val Ile Tyr Ser Leu Gln Arg Ala Leu Asp Cys Glu Leu Ala Glu Ala
563             245             250                 255
565 Gln Leu His Thr Thr Ala Ile Asp Lys Glu Gly Arg Arg Ala Val Lys
566             260             265                 270
568 Ala Gly Ala Tyr Ala Ala Cys Gln Glu Ala Lys Glu Asp Ile Lys Ser
569             275             280                 285
571 His Ser Glu Asn Val Ser Gln His Pro Leu His Val Glu Val Leu His
572     290             295                 300
574 Ser Glu Ile Met Ala His Gln Lys Phe Ala Leu Arg Leu Gly Ser Trp
575 305             310             315                 320
577 Met Asn Lys Ile Met Ser Tyr Ser Ser Asp Phe Arg Gln Ile Phe Cys
578             325             330                 335
580 Gln Ala Cys Leu Arg Glu Glu Pro Asp Ser Glu Asn Pro Cys Leu Ile
581             340             345                 350
583 Ser Arg Leu Met Leu Trp Asp Ala Lys Leu Tyr Lys Gly Ala Arg Lys
584             355             360                 365
586 Ile Leu His Glu Leu Ile Phe Ser Ser Phe Phe Met Glu Met Glu Tyr
587     370             375             380
589 Lys Lys Leu Phe Ala Met Glu Phe Val Lys Tyr Tyr Lys Gln Leu Gln
590 385             390             395                 400
592 Lys Glu Tyr Ile Ser Asp Asp His Asp Arg Ser Ile Ser Ile Thr Ala
593             405             410                 415
595 Leu Ser Val Gln Met Phe Thr Val Pro Thr Leu Ala Arg His Leu Ile
596             420             425                 430
598 Glu Glu Gln Asn Val Ile Ser Val Ile Thr Glu Thr Leu Leu Glu Val
599     435             440             445
601 Leu Pro Glu Tyr Leu Asp Arg Asn Asn Lys Phe Asn Phe Gln Gly Tyr
602     450             455             460
604 Ser Gln Asp Lys Leu Gly Arg Val Tyr Ala Val Ile Cys Asp Leu Lys
605 465             470             475                 480
607 Tyr Ile Leu Ile Ser Lys Pro Thr Ile Trp Thr Glu Arg Leu Arg Met
608             485             490                 495
610 Gln Phe Leu Glu Gly Phe Arg Ser Phe Leu Lys Ile Leu Thr Cys Met
611             500             505                 510
613 Gln Gly Met Glu Glu Ile Arg Arg Gln Val Gly Gln His Ile Glu Val
614             515             520                 525
616 Asp Pro Asp Trp Glu Ala Ala Ile Ala Ile Gln Met Gln Leu Lys Asn
617     530             535                 540
619 Ile Leu Leu Met Phe Gln Glu Trp Cys Ala Cys Asp Glu Glu Leu Leu
620 545             550             555                 560
622 Leu Val Ala Tyr Lys Glu Cys His Lys Ala Val Met Arg Cys Ser Thr
```

```
623                  565                  570                  575
625 Ser Phe Ile Ser Ser Ser Lys Thr Val Val Gln Ser Cys Gly His Ser
626                  580                  585                  590
628 Leu Glu Thr Lys Ser Tyr Arg Val Ser Glu Asp Leu Val Ser Ile His
629            595                  600                  605
631 Leu Pro Leu Ser Arg Thr Leu Ala Gly Leu His Val Arg Leu Ser Arg
632      610                  615                  620
634 Leu Gly Ala Val Ser Arg Leu His Glu Phe Val Ser Phe Glu Asp Phe
635 625                  630                  635                  640
637 Gln Val Glu Val Leu Val Glu Tyr Pro Leu Arg Cys Leu Val Leu Val
638                  645                  650                  655
640 Ala Gln Val Val Ala Glu Met Trp Arg Arg Asn Gly Leu Ser Leu Ile
641                  660                  665                  670
643 Ser Gln Val Phe Tyr Tyr Gln Asp Val Lys Cys Arg Glu Glu Met Tyr
644            675                  680                  685
646 Asp Lys Asp Ile Ile Met Leu Gln Ile Gly Ala Ser Leu Met Asp Pro
647      690                  695                  700
649 Asn Lys Phe Leu Leu Leu Val Leu Gln Arg Tyr Glu Leu Ala Glu Ala
650 705                  710                  715                  720
652 Phe Asn Lys Thr Ile Ser Thr Lys Asp Gln Asp Leu Ile Lys Gln Tyr
653                  725                  730                  735
655 Asn Thr Leu Ile Glu Glu Met Leu Gln Val Leu Ile Tyr Ile Val Gly
656            740                  745                  750
658 Glu Arg Tyr Val Pro Gly Val Gly Asn Val Thr Lys Glu Glu Val Thr
659            755                  760                  765
661 Met Arg Glu Ile Ile His Leu Leu Cys Ile Glu Pro Met Pro His Ser
662      770                  775                  780
664 Ala Ile Ala Lys Asn Leu Pro Glu Asn Glu Asn Asn Glu Thr Gly Leu
665 785                  790                  795                  800
667 Glu Asn Val Ile Asn Lys Val Ala Thr Phe Lys Lys Pro Gly Val Ser
668                  805                  810                  815
670 Gly His Gly Val Tyr Glu Leu Lys Asp Glu Ser Leu Lys Asp Phe Asn
671            820                  825                  830
673 Met Tyr Phe Tyr His Tyr Ser Lys Thr Gln His Ser Lys Ala Glu His
674            835                  840                  845
676 Met Gln Lys Lys Arg Arg Lys Gln Glu Asn Lys Asp Glu Ala Leu Pro
677      850                  855                  860
679 Pro Pro Pro Pro Glu Phe Cys Pro Ala Phe Ser Lys Val Ile Asn
680 865                  870                  875                  880
682 Leu Leu Asn Cys Asp Ile Met Met Tyr Ile Leu Arg Thr Val Phe Glu
683                  885                  890                  895
685 Arg Ala Ile Asp Thr Asp Ser Asn Leu Trp Thr Glu Gly Met Leu Gln
686            900                  905                  910
688 Met Ala Phe His Ile Leu Ala Leu Gly Leu Leu Glu Glu Lys Gln Gln
689            915                  920                  925
691 Leu Gln Lys Ala Pro Glu Glu Glu Val Thr Phe Asp Phe Tyr His Lys
692      930                  935                  940
694 Ala Ser Arg Leu Gly Ser Ser Ala Met Asn Ile Gln Met Leu Leu Glu
695 945                  950                  955                  960
```

```
697 Lys Leu Lys Gly Ile Pro Gln Leu Glu Gly Gln Lys Asp Met Ile Thr
698             965                   970                   975
700 Trp Ile Leu Gln Met Phe Asp Thr Val Lys Arg Leu Arg Glu Lys Ser
701             980                   985                   990
703 Cys Leu Ile Val Ala Thr Thr Ser Gly Ser Glu Ser Ile Lys Asn Asp
704            995                  1000                  1005
706 Glu Ile Thr His Asp Lys Glu Lys Ala Glu Arg Lys Arg Lys Ala Glu
707     1010                  1015                  1020
709 Ala Ala Arg Leu His Arg Gln Lys Ile Met Ala Gln Met Ser Ala Leu
E--> 710 (025) 1025         1030              1035              1040
712 Gln Lys Asn Phe Ile Glu Thr His Lys Leu Met Tyr Asp Asn Thr Ser
713             1045                  1050                  1055
715 Glu Met Pro Gly Lys Glu Asp Ser Ile Met Glu Glu Glu Ser Thr Pro
716             1060                  1065                  1070
718 Ala Val Ser Asp Tyr Ser Arg Ile Ala Leu Gly Pro Lys Arg Gly Pro
719             1075                  1080                  1085
721 Ser Val Thr Glu Lys Glu Val Leu Thr Cys Ile Leu Cys Gln Glu Glu
722     1090                  1095                  1100
724 Gln Glu Val Lys Ile Glu Asn Asn Ala Met Val Leu Ser Ala Cys Val
E--> 725 (105) 1105         1110              1115              1120
727 Gln Lys Ser Thr Ala Leu Thr Gln His Arg Gly Lys Pro Ile Glu Leu
728             1125                  1130                  1135
730 Ser Gly Glu Ala Leu Asp Pro Leu Phe Met Asp Pro Asp Leu Ala Tyr
731             1140                  1145                  1150
733 Gly Thr Tyr Thr Gly Ser Cys Gly His Val Met His Ala Val Cys Trp
734     1155                  1160                  1165
736 Gln Lys Tyr Phe Glu Ala Val Gln Leu Ser Ser Gln Gln Arg Ile His
737     1170                  1175                  1180
739 Val Asp Leu Phe Asp Leu Glu Ser Gly Glu Tyr Leu Cys Pro Leu Cys
E--> 740 (185) 1185         1190              1195              1200
742 Lys Ser Leu Cys Asn Thr Val Ile Pro Ile Ile Pro Leu Gln Pro Gln
743             1205                  1210                  1215
745 Lys Ile Asn Ser Glu Asn Ala Asp Ala Leu Ala Gln Leu Leu Thr Leu
746             1220                  1225                  1230
748 Ala Arg Trp Ile Gln Thr Val Leu Ala Arg Ile Ser Gly Tyr Asn Ile
749     1235                  1240                  1245
751 Arg His Ala Lys Gly Glu Asn Pro Ile Pro Ile Phe Phe Asn Gln Gly
752     1250                  1255                  1260
754 Met Gly Asp Ser Thr Leu Glu Phe His Ser Ile Leu Ser Phe Gly Val
E--> 755 (265) 1265         1270              1275              1280
757 Glu Ser Ser Ile Lys Tyr Ser Asn Ser Ile Lys Glu Met Val Ile Leu
758             1285                  1290                  1295
760 Phe Ala Thr Thr Ile Tyr Arg Ile Gly Leu Lys Val Pro Pro Asp Glu
761     1300                  1305                  1310
763 Arg Asp Pro Arg Val Pro Met Leu Thr Trp Ser Thr Cys Ala Phe Thr
764     1315                  1320                  1325
766 Ile Gln Ala Ile Glu Asn Leu Leu Gly Asp Glu Gly Lys Pro Leu Phe
767     1330                  1335                  1340
769 Gly Ala Leu Gln Asn Arg Gln His Asn Gly Leu Lys Ala Leu Met Gln
```

[Handwritten margin note:] When numbering the first amino acid on a line, begin the number directly under the first letter of the amino acid

e.g. Ala 1025 [space] Ala

```
E--> 770 (345)              1350              1355              1360
     772 Phe Ala Val Ala Gln Arg Ile Thr Cys Pro Gln Val Leu Ile Gln Lys
     773          1365              1370              1375
     775 His Leu Val Arg Leu Leu Ser Val Val Leu Pro Asn Ile Lys Ser Glu
     776          1380              1385              1390
     778 Asp Thr Pro Cys Leu Leu Ser Ile Asp Leu Phe His Val Leu Val Gly
     779          1395              1400              1405
     781 Ala Val Leu Ala Phe Pro Ser Leu Tyr Trp Asp Asp Pro Val Asp Leu
     782    1410              1415              1420
     784 Gln Pro Ser Ser Val Ser Ser Ser Tyr Asn His Leu Tyr Leu Phe His
E--> 785 (425)              1430              1435              1440
     787 Leu Ile Thr Met Ala His Met Leu Gln Ile Leu Leu Thr Val Asp Thr
     788          1445              1450              1455
     790 Gly Leu Pro Leu Ala Gln Val Gln Glu Asp Ser Glu Glu Ala His Ser
     791          1460              1465              1470
     793 Ala Ser Ser Phe Phe Ala Glu Ile Ser Gln Tyr Thr Ser Gly Ser Ile
     794          1475              1480              1485
     796 Gly Cys Asp Ile Pro Gly Trp Tyr Leu Trp Val Ser Leu Lys Asn Gly
     797    1490              1495              1500
     799 Ile Thr Pro Tyr Leu Arg Cys Ala Ala Leu Phe Phe His Tyr Leu Leu
E--> 800 (505)              1510              1515              1520
     802 Gly Val Thr Pro Pro Glu Glu Leu His Thr Asn Ser Ala Glu Gly Glu
     803          1525              1530              1535
     805 Tyr Ser Ala Leu Cys Ser Tyr Leu Ser Leu Pro Thr Asn Leu Phe Leu
     806          1540              1545              1550
     808 Leu Phe Gln Glu Tyr Trp Asp Thr Val Arg Pro Leu Leu Gln Arg Trp
     809          1555              1560              1565
     811 Cys Ala Asp Pro Ala Leu Leu Asn Cys Leu Lys Gln Lys Asn Thr Val
     812    1570              1575              1580
     814 Val Arg Tyr Pro Arg Lys Arg Asn Ser Leu Ile Glu Leu Pro Asp Asp
E--> 815 (585)              1590              1595              1600
     817 Tyr Ser Cys Leu Leu Asn Gln Ala Ser His Phe Arg Cys Pro Arg Ser
     818          1605              1610              1615
     820 Ala Asp Asp Glu Arg Lys His Pro Val Leu Cys Leu Phe Cys Gly Ala
     821          1620              1625              1630
     823 Ile Leu Cys Ser Gln Asn Ile Cys Cys Gln Glu Ile Val Asn Gly Glu
     824          1635              1640              1645
     826 Glu Val Gly Ala Cys Ile Phe His Ala Leu His Cys Gly Ala Gly Val
     827    1650              1655              1660
     829 Cys Ile Phe Leu Lys Ile Arg Glu Cys Arg Val Val Leu Val Glu Gly
E--> 830 (665)              1670              1675              1680
     832 Lys Ala Arg Gly Cys Ala Tyr Pro Ala Pro Tyr Leu Asp Glu Tyr Gly
     833          1685              1690              1695
     835 Glu Thr Asp Pro Gly Leu Lys Arg Gly Asn Pro Leu His Leu Ser Arg
     836          1700              1705              1710
     838 Glu Arg Tyr Arg Lys Leu His Leu Val Trp Gln Gln His Cys Ile Ile
     839          1715              1720              1725
     841 Glu Glu Ile Ala Arg Ser Gln Glu Thr Asn Gln Met Leu Phe Gly Phe
     842    1730              1735              1740
```

Input Set : A:\35966C.txt
Output Set: N:\CRF4\01272004\J758636.raw

```
    844 Asn Trp Gln Leu Leu
E--> 845 (745)
   1338 <210> SEQ ID NO: 4
   1339 <211> LENGTH: 1755
   1340 <212> TYPE: PRT
   1341 <213> ORGANISM: Homo sapiens
   1343 <400> SEQUENCE: 4
   1344 Met Ala Ser Glu Leu Glu Pro Glu Val Gln Ala Ile Asp Arg Ser Leu
   1345   1               5                  10                  15
   1347 Leu Glu Cys Ser Ala Glu Glu Ile Ala Gly Lys Trp Leu Gln Ala Thr
   1348              20                  25                  30
   1350 Asp Leu Thr Arg Glu Val Tyr Gln His Leu Ala His Tyr Val Pro Lys
   1351          35                  40                  45
   1353 Ile Tyr Cys Arg Gly Pro Asn Pro Phe Pro Gln Lys Glu Asp Met Leu
   1354      50                  55                  60
   1356 Ala Gln His Val Leu Leu Gly Pro Met Glu Trp Tyr Leu Cys Gly Glu
   1357  65                  70                  75                  80
   1359 Asp Pro Ala Phe Gly Phe Pro Lys Leu Glu Gln Ala Asn Lys Pro Ser
   1360              85                  90                  95
   1362 His Leu Cys Gly Arg Val Phe Lys Val Gly Glu Pro Thr Tyr Ser Cys
   1363             100                 105                 110
   1365 Arg Asp Cys Ala Val Asp Pro Thr Cys Val Leu Cys Met Glu Cys Phe
   1366          115                 120                 125
   1368 Leu Gly Ser Ile His Arg Asp His Arg Tyr Arg Met Thr Thr Ser Gly
   1369      130                 135                 140
   1371 Gly Gly Gly Phe Cys Asp Cys Gly Asp Thr Glu Ala Trp Lys Glu Gly
   1372 145                 150                 155                 160
   1374 Pro Tyr Cys Gln Lys His Glu Leu Asn Thr Ser Glu Ile Glu Glu Glu
   1375             165                 170                 175
   1377 Glu Asp Pro Leu Val His Leu Ser Glu Asp Val Ile Ala Arg Thr Tyr
   1378             180                 185                 190
   1380 Asn Ile Phe Ala Ile Thr Phe Arg Tyr Ala Val Glu Ile Leu Thr Trp
   1381          195                 200                 205
   1383 Glu Lys Glu Ser Glu Leu Pro Ala Asp Leu Glu Met Val Glu Lys Ser
   1384      210                 215                 220
   1386 Asp Thr Tyr Tyr Cys Met Leu Phe Asn Asp Glu Val His Thr Tyr Glu
   1387 225                 230                 235                 240
   1389 Gln Val Ile Tyr Thr Leu Gln Lys Ala Val Asn Cys Thr Gln Lys Glu
   1390             245                 250                 255
   1392 Ala Ile Gly Phe Ala Thr Thr Val Asp Arg Asp Gly Arg Arg Ser Val
   1393          260                 265                 270
   1395 Arg Tyr Gly Asp Phe Gln Tyr Cys Glu Gln Ala Lys Ser Val Ile Val
   1396          275                 280                 285
   1398 Arg Asn Thr Ser Arg Gln Thr Lys Pro Leu Lys Val Gln Val Met His
   1399          290                 295                 300
   1401 Ser Ser Ile Val Ala His Gln Asn Phe Gly Leu Lys Leu Leu Ser Trp
   1402 305                 310                 315                 320
   1404 Leu Gly Ser Ile Ile Gly Tyr Ser Asp Gly Leu Arg Arg Ile Leu Cys
   1405             325                 330                 335
```

RAW SEQUENCE LISTING
PATENT APPLICATION: **US/10/758,636**

Input Set : **A:\35966C.txt**
Output Set: **N:\CRF4\01272004\J758636.raw**

```
1407 Gln Val Gly Leu Gln Glu Gly Pro Asp Gly Glu Asn Ser Ser Leu Val
1408             340                 345                 350
1410 Asp Arg Leu Met Leu Ser Asp Ser Lys Leu Trp Lys Gly Ala Arg Ser
1411         355                 360                 365
1413 Val Tyr His Gln Leu Phe Met Ser Ser Leu Leu Met Asp Leu Lys Tyr
1414     370                 375                 380
1416 Lys Lys Leu Phe Ala Val Arg Phe Ala Lys Asn Tyr Gln Gln Leu Gln
1417 385                 390                 395                 400
1419 Arg Asp Phe Met Glu Asp Asp His Glu Arg Ala Val Ser Val Thr Ala
1420             405                 410                 415
1422 Leu Ser Val Gln Phe Phe Thr Ala Pro Thr Leu Ala Arg Met Leu Ile
1423             420                 425                 430
1425 Thr Glu Glu Asn Leu Met Ser Ile Ile Ile Lys Thr Phe Met Asp His
1426         435                 440                 445
1428 Leu Arg His Arg Asp Ala Gln Gly Arg Phe Gln Phe Glu Arg Tyr Thr
1429     450                 455                 460
1431 Ala Leu Gln Ala Phe Lys Phe Arg Arg Val Gln Ser Leu Ile Leu Asp
1432 465                 470                 475                 480
1434 Leu Lys Tyr Val Leu Ile Ser Lys Pro Thr Glu Trp Ser Asp Glu Leu
1435             485                 490                 495
1437 Arg Gln Lys Phe Leu Glu Gly Phe Asp Ala Phe Leu Glu Leu Leu Lys
1438         500                 505                 510
1440 Cys Met Gln Gly Met Asp Pro Ile Thr Arg Gln Val Gly Gln His Ile
1441         515                 520                 525
1443 Glu Met Glu Pro Glu Trp Glu Ala Ala Phe Thr Leu Gln Met Lys Leu
1444     530                 535                 540
1446 Thr His Val Ile Ser Met Met Gln Asp Trp Cys Ala Ser Asp Glu Lys
1447 545                 550                 555                 560
1449 Val Leu Ile Glu Ala Tyr Lys Lys Cys Leu Ala Val Leu Met Gln Cys
1450             565                 570                 575
1452 His Gly Gly Tyr Thr Asp Gly Glu Gln Pro Ile Thr Leu Ser Ile Cys
1453         580                 585                 590
1455 Gly His Ser Val Glu Thr Ile Arg Tyr Cys Val Ser Gln Glu Lys Val
1456     595                 600                 605
1458 Ser Ile His Leu Pro Val Ser Arg Leu Leu Ala Gly Leu His Val Leu
1459     610                 615                 620
1461 Leu Ser Lys Ser Glu Val Ala Tyr Lys Phe Pro Glu Leu Leu Pro Leu
1462 625                 630                 635                 640
1464 Ser Glu Leu Ser Pro Pro Met Leu Ile Glu His Pro Leu Arg Cys Leu
1465                 645                 650                 655
1467 Val Leu Cys Ala Gln Val His Ala Gly Met Trp Arg Arg Asn Gly Phe
1468             660                 665                 670
1470 Ser Leu Val Asn Gln Ile Tyr Tyr Tyr His Asn Val Lys Cys Arg Arg
1471         675                 680                 685
1473 Glu Met Phe Asp Lys Asp Val Val Met Leu Gln Thr Gly Val Ser Met
1474     690                 695                 700
1476 Met Asp Pro Asn His Phe Leu Met Ile Met Leu Ser Arg Phe Glu Leu
1477 705                 710                 715                 720
1479 Tyr Gln Ile Phe Ser Thr Pro Asp Tyr Gly Lys Arg Phe Ser Ser Glu
```

RAW SEQUENCE LISTING   DATE: 01/27/2004
PATENT APPLICATION: US/10/758,636   TIME: 10:59:30

Input Set : A:\35966C.txt
Output Set: N:\CRF4\01272004\J758636.raw

```
1480                  725                  730                  735
1482 Ile Thr His Lys Asp Val Val Gln Gln Asn Asn Thr Leu Ile Glu Glu
1483          740                  745                  750
1485 Met Leu Tyr Leu Ile Ile Met Leu Val Gly Glu Arg Phe Ser Pro Gly
1486          755                  760                  765
1488 Val Gly Gln Val Asn Ala Thr Asp Glu Ile Lys Arg Glu Ile Ile His
1489     770                  775                  780
1491 Gln Leu Ser Ile Lys Pro Met Ala His Ser Glu Leu Val Lys Ser Leu
1492 785                  790                  795                  800
1494 Pro Glu Asp Glu Asn Lys Glu Thr Gly Met Glu Ser Val Ile Glu Ala
1495                  805                  810                  815
1497 Val Ala His Phe Lys Lys Pro Gly Leu Thr Gly Arg Gly Met Tyr Glu
1498              820                  825                  830
1500 Leu Lys Pro Glu Cys Ala Lys Glu Phe Asn Leu Tyr Phe Tyr His Phe
1501          835                  840                  845
1503 Ser Arg Ala Glu Gln Ser Lys Ala Glu Glu Ala Gln Arg Lys Leu Lys
1504     850                  855                  860
1506 Arg Gln Asn Arg Glu Asp Thr Ala Leu Pro Pro Pro Val Leu Pro Pro
1507 865                  870                  875                  880
1509 Phe Cys Pro Leu Phe Ala Ser Leu Val Asn Ile Leu Gln Ser Asp Val
1510                  885                  890                  895
1512 Met Leu Cys Ile Met Gly Thr Ile Leu Gln Trp Ala Val Glu His Asn
1513              900                  905                  910
1515 Gly Tyr Ala Trp Ser Glu Ser Met Leu Gln Arg Val Leu His Leu Ile
1516          915                  920                  925
1518 Gly Met Ala Leu Gln Glu Glu Lys Gln His Leu Glu Asn Val Thr Glu
1519     930                  935                  940
1521 Glu His Val Val Thr Phe Thr Phe Thr Gln Lys Ile Ser Lys Pro Gly
1522 945                  950                  955                  960
1524 Glu Ala Pro Lys Asn Ser Pro Ser Ile Leu Ala Met Leu Glu Thr Leu
1525              965                  970                  975
1527 Gln Asn Ala Pro Tyr Leu Glu Val His Lys Asp Met Ile Arg Trp Ile
1528          980                  985                  990
1530 Leu Lys Thr Phe Asn Ala Val Lys Lys Met Arg Glu Ser Ser Pro Thr
1531          995                  1000                 1005
1533 Ser Pro Val Ala Glu Thr Glu Gly Thr Ile Met Glu Glu Ser Ser Arg
1534     1010                 1015                 1020
1536 Asp Lys Asp Lys Ala Glu Arg Lys Arg Lys Ala Glu Ile Ala Arg Leu
```
E--> 1537 (025)/025   1030   1035   1040
```
1539 Arg Arg Glu Lys Ile Met Ala Gln Met Ser Glu Met Gln Arg His Phe
1540          1045                 1050                 1055
1542 Ile Asp Glu Asn Lys Glu Leu Phe Gln Gln Thr Leu Glu Leu Asp Ala
1543          1060                 1065                 1070
1545 Ser Thr Ser Ala Val Leu Asp His Ser Pro Val Ala Ser Asp Met Thr
1546          1075                 1080                 1085
1548 Leu Thr Ala Leu Gly Pro Thr Gln Thr Gln Val Pro Glu Gln Arg Gln
1549     1090                 1095                 1100
1551 Phe Val Thr Cys Ile Leu Cys Gln Glu Glu Gln Glu Val Lys Val Glu
```
E--> 1552 (105)/105   1110   1115   1120

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```
1554 Ser Arg Ala Met Val Leu Ala Ala Phe Val Gln Arg Ser Thr Val Leu
1555           1125           1130           1135
1557 Ser Lys Asn Arg Ser Lys Phe Ile Gln Asp Pro Glu Lys Tyr Asp Pro
1558           1140           1145           1150
1560 Leu Phe Met His Pro Asp Leu Ser Cys Gly Thr His Thr Ser Ser Cys
1561           1155           1160           1165
1563 Gly His Ile Met His Ala His Cys Trp Gln Arg Tyr Phe Asp Ser Val
1564      1170           1175           1180
1566 Gln Ala Lys Glu Gln Arg Arg Gln Gln Arg Leu Arg Leu His Thr Ser
```
E--> 1567 (185) //85   1190   1195   1200
```
1569 Tyr Asp Val Glu Asn Gly Glu Phe Leu Cys Pro Leu Cys Glu Cys Leu
1570           1205           1210           1215
1572 Ser Asn Thr Val Ile Pro Leu Leu Leu Pro Pro Arg Asn Ile Phe Asn
1573           1220           1225           1230
1575 Asn Arg Leu Asn Phe Ser Asp Gln Pro Asn Leu Thr Gln Trp Ile Arg
1576      1235           1240           1245
1578 Thr Ile Ser Gln Gln Ile Lys Ala Leu Gln Phe Leu Arg Lys Glu Glu
1579      1250           1255           1260
1581 Ser Thr Pro Asn Asn Ala Ser Thr Lys Asn Ser Glu Asn Val Asp Glu
```
E--> 1582 (265)/265   1270   1275   1280
```
1584 Leu Gln Leu Pro Glu Gly Phe Arg Pro Asp Phe Arg Pro Lys Ile Pro
1585           1285           1290           1295
1587 Tyr Ser Glu Ser Ile Lys Glu Met Leu Thr Thr Phe Gly Thr Ala Thr
1588           1300           1305           1310
1590 Tyr Lys Val Gly Leu Lys Val His Pro Asn Glu Glu Asp Pro Arg Val
1591      1315           1320           1325
1593 Pro Ile Met Cys Trp Gly Ser Cys Ala Tyr Thr Ile Gln Ser Ile Glu
1594      1330           1335           1340
1596 Arg Ile Leu Ser Asp Glu Asp Lys Pro Leu Phe Gly Pro Leu Pro Cys
```
E--> 1597 (345)/345   1350   1355   1360
```
1599 Arg Leu Asp Asp Cys Leu Arg Ser Leu Thr Arg Phe Ala Ala Ala His
1600           1365           1370           1375
1602 Trp Thr Val Ala Ser Val Ser Val Val Gln Gly His Phe Cys Lys Leu
1603           1380           1385           1390
1605 Phe Ala Ser Leu Val Pro Asn Asp Ser His Glu Glu Leu Pro Cys Ile
1606      1395           1400           1405
1608 Leu Asp Ile Asp Met Phe His Leu Leu Val Gly Leu Val Leu Ala Phe
1609      1410           1415           1420
1611 Pro Ala Leu Gln Cys Gln Asp Phe Ser Gly Ile Ser Leu Gly Thr Gly
```
E--> 1612 (425)/425   1430   1435   1440
```
1614 Asp Leu His Ile Phe His Leu Val Thr Met Ala His Ile Ile Gln Ile
1615           1445           1450           1455
1617 Leu Leu Thr Ser Cys Thr Glu Glu Asn Gly Met Asp Gln Glu Asn Pro
1618           1460           1465           1470
1620 Pro Cys Glu Glu Glu Ser Ala Val Leu Ala Leu Tyr Lys Thr Leu His
1621      1475           1480           1485
1623 Gln Tyr Thr Gly Ser Ala Leu Lys Glu Ile Pro Ser Gly Trp His Leu
1624      1490           1495           1500
1626 Trp Arg Ser Val Arg Ala Gly Ile Met Pro Phe Leu Lys Cys Ser Ala
```

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E--> 1627 505   1510   1515   1520
1629 Leu Phe Phe His Tyr Leu Asn Gly Val Pro Ser Pro Pro Asp Ile Gln
1630   1525   1530   1535
1632 Val Pro Gly Thr Ser His Phe Glu His Leu Cys Ser Tyr Leu Ser Leu
1633   1540   1545   1550
1635 Pro Asn Asn Leu Ile Cys Leu Phe Gln Glu Asn Ser Glu Ile Met Asn
1636   1555   1560   1565
1638 Ser Leu Ile Glu Ser Trp Cys Arg Asn Ser Glu Val Lys Arg Tyr Leu
1639   1570   1575   1580
1641 Glu Gly Glu Arg Asp Ala Ile Arg Tyr Pro Arg Glu Ser Asn Lys Leu
E--> 1642 585   1590   1595   1600
1644 Ile Asn Leu Pro Glu Asp Tyr Ser Ser Leu Ile Asn Gln Ala Ser Asn
1645   1605   1610   1615
1647 Phe Ser Cys Pro Lys Ser Gly Gly Asp Lys Ser Arg Ala Pro Thr Leu
1648   1620   1625   1630
1650 Cys Leu Val Cys Gly Ser Leu Leu Cys Ser Gln Ser Tyr Cys Cys Gln
1651   1635   1640   1645
1653 Thr Glu Leu Glu Gly Glu Asp Val Gly Ala Cys Thr Ala His Thr Tyr
1654   1650   1655   1660
1656 Ser Cys Gly Ser Gly Val Gly Ile Phe Leu Arg Val Arg Glu Cys Gln
E--> 1657 665   1670   1675   1680
1659 Val Leu Phe Leu Ala Gly Lys Thr Lys Gly Cys Phe Tyr Ser Pro Pro
1660   1685   1690   1695
1662 Tyr Leu Asp Asp Tyr Gly Glu Thr Asp Gln Gly Leu Arg Arg Gly Asn
1663   1700   1705   1710
1665 Pro Leu His Leu Cys Lys Glu Arg Phe Lys Lys Ile Gln Lys Leu Trp
1666   1715   1720   1725
1668 His Gln His Ser Val Thr Glu Glu Ile Gly His Ala Gln Glu Ala Asn
1669   1730   1735   1740
1671 Gln Thr Leu Val Gly Ile Asp Trp Gln His Leu
E--> 1672 745   1750   1755
2157 <210> SEQ ID NO: 6
2158 <211> LENGTH: 1755
2159 <212> TYPE: PRT
2160 <213> ORGANISM: Mouse
2162 <400> SEQUENCE: 6
2163 Met Ala Ser Glu Met Glu Pro Glu Val Gln Ala Ile Asp Arg Ser Leu
2164   1   5   10   15
2166 Leu Glu Cys Ser Ala Glu Glu Ile Ala Gly Arg Trp Leu Gln Ala Thr
2167   20   25   30
2169 Asp Leu Asn Arg Glu Val Tyr Gln His Leu Ala His Cys Val Pro Lys
2170   35   40   45
2172 Ile Tyr Cys Arg Gly Pro Asn Pro Phe Pro Gln Lys Glu Asp Thr Leu
2173   50   55   60
2175 Ala Gln His Ile Leu Leu Gly Pro Met Glu Trp Tyr Ile Cys Ala Glu
2176 65   70   75   80
2178 Asp Pro Ala Leu Gly Phe Pro Lys Leu Glu Gln Ala Asn Lys Pro Ser
2179   85   90   95
2181 His Leu Cys Gly Arg Val Phe Lys Val Gly Glu Pro Thr Tyr Ser Cys

pr 13-15

```
2182              100              105              110
2184 Arg Asp Cys Ala Val Asp Pro Thr Cys Val Leu Cys Met Glu Cys Phe
2185          115              120              125
2187 Leu Gly Ser Ile His Arg Asp His Arg Tyr Arg Met Thr Thr Ser Gly
2188      130              135              140
2190 Gly Gly Gly Phe Cys Asp Cys Gly Asp Thr Glu Ala Trp Lys Glu Gly
2191 145              150              155              160
2193 Pro Tyr Cys Gln Lys His Lys Leu Ser Ser Ser Glu Val Val Glu Glu
2194              165              170              175
2196 Glu Asp Pro Leu Val His Leu Ser Glu Asp Val Ile Ala Arg Thr Tyr
2197              180              185              190
2199 Asn Ile Phe Ala Ile Met Phe Arg Tyr Ala Val Asp Ile Leu Thr Trp
2200          195              200              205
2202 Glu Lys Glu Ser Glu Leu Pro Glu Asp Leu Glu Val Ala Glu Lys Ser
2203      210              215              220
2205 Asp Thr Tyr Tyr Cys Met Leu Phe Asn Asp Glu Val His Thr Tyr Glu
2206 225              230              235              240
2208 Gln Val Ile Tyr Thr Leu Gln Lys Ala Val Asn Cys Thr Gln Lys Glu
2209              245              250              255
2211 Ala Ile Gly Phe Ala Thr Thr Val Asp Arg Asp Gly Arg Arg Pro Val
2212          260              265              270
2214 Arg Tyr Gly Asp Phe Gln Tyr Cys Asp Gln Ala Lys Thr Val Ile Val
2215      275              280              285
2217 Arg Asn Thr Ser Arg Gln Thr Lys Pro Leu Lys Val Gln Val Met His
2218      290              295              300
2220 Ser Ser Val Ala Ala His Gln Asn Phe Gly Leu Lys Ala Leu Ser Trp
2221 305              310              315              320
2223 Leu Gly Ser Val Ile Gly Tyr Ser Asp Gly Leu Arg Arg Ile Leu Cys
2224          325              330              335
2226 Gln Val Gly Leu Gln Glu Gly Pro Asp Gly Glu Asn Ser Ser Leu Val
2227          340              345              350
2229 Asp Arg Leu Met Leu Asn Asp Ser Lys Leu Trp Lys Gly Ala Arg Ser
2230      355              360              365
2232 Val Tyr His Gln Leu Phe Met Ser Ser Leu Leu Met Asp Leu Lys Tyr
2233      370              375              380
2235 Lys Lys Leu Phe Ala Leu Arg Phe Ala Lys Asn Tyr Arg Gln Leu Gln
2236 385              390              395              400
2238 Arg Asp Phe Met Glu Asp Asp His Glu Arg Ala Val Ser Val Thr Ala
2239              405              410              415
2241 Leu Ser Val Gln Phe Phe Thr Ala Pro Thr Leu Ala Arg Met Leu Leu
2242          420              425              430
2244 Thr Glu Glu Asn Leu Met Thr Val Ile Ile Lys Ala Phe Met Asp His
2245      435              440              445
2247 Leu Lys His Arg Asp Ala Gln Gly Arg Phe Gln Phe Glu Arg Tyr Thr
2248      450              455              460
2250 Ala Leu Gln Ala Phe Lys Phe Arg Arg Val Gln Ser Leu Ile Leu Asp
2251 465              470              475              480
2253 Leu Lys Tyr Val Leu Ile Ser Lys Pro Thr Glu Trp Ser Asp Glu Leu
2254              485              490              495
```

```
2256 Arg Gln Lys Phe Leu Gln Gly Phe Asp Ala Phe Leu Glu Leu Leu Lys
2257         500                 505                 510
2259 Cys Met Gln Gly Met Asp Pro Ile Thr Arg Gln Val Gly Gln His Ile
2260         515                 520                 525
2262 Glu Met Glu Pro Glu Trp Glu Ala Ala Phe Thr Leu Gln Met Lys Leu
2263         530                 535                 540
2265 Thr His Val Ile Ser Met Val Gln Asp Trp Cys Ala Leu Asp Glu Lys
2266 545                 550                 555                 560
2268 Val Leu Ile Glu Ala Tyr Lys Lys Cys Leu Ala Val Leu Thr Gln Cys
2269                 565                 570                 575
2271 His Gly Gly Phe Thr Asp Gly Glu Gln Pro Ile Thr Leu Ser Ile Cys
2272             580                 585                 590
2274 Gly His Ser Val Glu Thr Ile Arg Tyr Cys Val Ser Gln Glu Lys Val
2275         595                 600                 605
2277 Ser Ile His Leu Pro Ile Ser Arg Leu Leu Ala Gly Leu His Val Leu
2278     610                 615                 620
2280 Leu Ser Lys Ser Glu Val Ala Tyr Lys Phe Pro Glu Leu Leu Pro Leu
2281 625                 630                 635                 640
2283 Ser Glu Leu Ser Pro Pro Met Leu Ile Glu His Pro Leu Arg Cys Leu
2284                 645                 650                 655
2286 Val Leu Cys Ala Gln Val His Ala Gly Met Trp Arg Arg Asn Gly Phe
2287             660                 665                 670
2289 Ser Leu Val Asn Gln Ile Tyr Tyr Tyr His Asn Val Lys Cys Arg Arg
2290         675                 680                 685
2292 Glu Met Phe Asp Lys Asp Ile Val Met Leu Gln Thr Gly Val Ser Met
2293     690                 695                 700
2295 Met Asp Pro Asn His Phe Leu Met Ile Met Leu Ser Arg Phe Glu Leu
2296 705                 710                 715                 720
2298 Tyr Gln Leu Phe Ser Thr Pro Asp Tyr Gly Lys Arg Phe Ser Ser Glu
2299             725                 730                 735
2301 Val Thr His Lys Asp Val Val Gln Gln Asn Asn Thr Leu Ile Glu Glu
2302             740                 745                 750
2304 Met Leu Tyr Leu Ile Ile Met Leu Val Gly Glu Arg Phe Asn Pro Gly
2305         755                 760                 765
2307 Val Gly Gln Val Ala Ala Thr Asp Glu Ile Lys Arg Glu Ile Ile His
2308     770                 775                 780
2310 Gln Leu Ser Ile Lys Pro Met Ala His Ser Glu Leu Val Lys Ser Leu
2311 785                 790                 795                 800
2313 Pro Glu Asp Glu Asn Lys Glu Thr Gly Met Glu Ser Val Ile Glu Ser
2314             805                 810                 815
2316 Val Ala His Phe Lys Lys Pro Gly Leu Thr Gly Arg Gly Met Tyr Glu
2317             820                 825                 830
2319 Leu Lys Pro Glu Cys Ala Lys Glu Phe Asn Leu Tyr Phe Tyr His Phe
2320         835                 840                 845
2322 Ser Arg Ala Glu Gln Ser Lys Ala Glu Glu Ala Gln Arg Lys Leu Lys
2323     850                 855                 860
2325 Arg Glu Asn Lys Glu Asp Thr Ala Leu Pro Pro Pro Ala Leu Pro Pro
2326 865                 870                 875                 880
2328 Phe Cys Pro Leu Phe Ala Ser Leu Val Asn Ile Leu Gln Cys Asp Val
```

```
2329                     885               890                895
2331 Met Leu Tyr Ile Met Gly Thr Ile Leu Gln Trp Ala Val Glu His His
2332              900               905               910
2334 Gly Ser Ala Trp Ser Glu Ser Met Leu Gln Arg Val Leu His Leu Ile
2335              915               920               925
2337 Gly Met Ala Leu Gln Glu Glu Lys His His Leu Glu Asn Ala Val Glu
2338         930               935               940
2340 Gly His Val Gln Thr Phe Thr Phe Thr Gln Lys Ile Ser Lys Pro Gly
2341 945               950               955               960
2343 Asp Ala Pro His Asn Ser Pro Ser Ile Leu Ala Met Leu Glu Thr Leu
2344              965               970               975
2346 Gln Asn Ala Pro Ser Leu Glu Ala His Lys Asp Met Ile Arg Trp Leu
2347              980               985               990
2349 Leu Lys Met Phe Asn Ala Ile Lys Lys Ile Arg Glu Cys Ser Ser Ser
2350         995               1000              1005
2352 Ser Pro Val Ala Glu Ala Glu Gly Thr Ile Met Glu Glu Ser Ser Arg
2353    1010              1015              1020
2355 Asp Lys Asp Lys Ala Glu Arg Lys Arg Lys Ala Glu Ile Ala Arg Leu
E--> 2356(025)/025           1030              1035              1040
2358 Arg Arg Glu Lys Ile Met Ala Gln Met Ser Glu Met Gln Arg His Phe
2359              1045              1050              1055
2361 Ile Asp Glu Asn Lys Glu Leu Phe Gln Gln Thr Leu Glu Leu Asp Thr
2362         1060              1065              1070
2364 Ser Ala Ser Ala Thr Leu Asp Ser Ser Pro Pro Val Ser Asp Ala Ala
2365    1075              1080              1085
2367 Leu Thr Ala Leu Gly Pro Ala Gln Thr Gln Val Pro Glu Pro Arg Gln
2368    1090              1095              1100
2370 Phe Val Thr Cys Ile Leu Cys Gln Glu Glu Gln Glu Val Thr Val Gly
E--> 2371(105)              1110              1115              1120
2373 Ser Arg Ala Met Val Leu Ala Ala Phe Val Gln Arg Ser Thr Val Leu
2374              1125              1130              1135
2376 Ser Lys Asp Arg Thr Lys Thr Ile Ala Asp Pro Glu Lys Tyr Asp Pro
2377         1140              1145              1150
2379 Leu Phe Met His Pro Asp Leu Ser Cys Gly Thr His Thr Gly Ser Cys
2380    1155              1160              1165
2382 Gly His Val Met His Ala His Cys Trp Gln Arg Tyr Phe Asp Ser Val
2383    1170              1175              1180
2385 Gln Ala Lys Glu Gln Arg Arg Gln Gln Arg Leu Arg Leu His Thr Ser
E--> 2386(185)              1190              1195              1200
2388 Tyr Asp Val Glu Asn Gly Glu Phe Leu Cys Pro Leu Cys Glu Cys Leu
2389              1205              1210              1215
2391 Ser Asn Thr Val Ile Pro Leu Leu Leu Pro Pro Arg Ser Ile Leu Ser
2392         1220              1225              1230
2394 Arg Arg Leu Asn Phe Ser Asp Gln Pro Asp Leu Ala Gln Trp Thr Arg
2395    1235              1240              1245
2397 Ala Val Thr Gln Gln Ile Lys Val Val Gln Met Leu Arg Arg Lys His
2398    1250              1255              1260
2400 Asn Ala Ala Asp Thr Ser Ser Ser Glu Asp Thr Glu Ala Met Asn Ile
E--> 2401 265              1270              1275              1280
```

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```
      2403 Ile Pro Ile Pro Glu Gly Phe Arg Pro Asp Phe Tyr Pro Arg Asn Pro
      2404               1285          1290              1295
      2406 Tyr Ser Asp Ser Ile Lys Glu Met Leu Thr Thr Phe Gly Thr Ala Ala
      2407               1300              1305              1310
      2409 Tyr Lys Val Gly Leu Lys Val His Pro Asn Glu Gly Asp Pro Arg Val
      2410          1315              1320              1325
      2412 Pro Ile Leu Cys Trp Gly Thr Cys Ala Tyr Thr Ile Gln Ser Ile Glu
      2413      1330              1335              1340
      2415 Arg Ile Leu Ser Asp Glu Glu Lys Pro Val Phe Gly Pro Leu Pro Cys
E--> 2416 (345)              1350              1355              1360
      2418 Arg Leu Asp Asp Cys Leu Arg Ser Leu Thr Arg Phe Ala Ala Ala His
      2419               1365              1370              1375
      2421 Trp Thr Val Ala Leu Leu Pro Val Val Gln Gly His Phe Cys Lys Leu
      2422          1380              1385              1390
      2424 Phe Ala Ser Leu Val Pro Ser Asp Ser Tyr Glu Asp Leu Pro Cys Ile
      2425          1395              1400              1405
      2427 Leu Asp Ile Asp Met Phe His Leu Leu Val Gly Leu Val Leu Ala Phe
      2428      1410              1415              1420
      2430 Pro Ala Leu Gln Cys Gln Asp Phe Ser Gly Ser Ser Leu Ala Thr Gly
E--> 2431 (425)              1430              1435              1440
      2433 Asp Leu His Ile Phe His Leu Val Thr Met Ala His Ile Val Gln Ile
      2434               1445              1450              1455
      2436 Leu Leu Thr Ser Cys Thr Glu Glu Asn Gly Met Asp Gln Glu Asn Pro
      2437          1460              1465              1470
      2439 Thr Gly Glu Glu Glu Leu Ala Ile Leu Ser Leu His Lys Thr Leu His
      2440          1475              1480              1485
      2442 Gln Tyr Thr Gly Ser Ala Leu Lys Glu Ala Pro Ser Gly Trp His Leu
      2443      1490              1495              1500
      2445 Trp Arg Ser Val Arg Ala Ala Ile Met Pro Phe Leu Lys Cys Ser Ala
E--> 2446 (505)              1510              1515              1520
      2448 Leu Phe Phe His Tyr Leu Asn Gly Val Pro Ala Pro Pro Asp Leu Gln
      2449               1525              1530              1535
      2451 Val Ser Gly Thr Ser His Phe Glu His Leu Cys Asn Tyr Leu Ser Leu
      2452          1540              1545              1550
      2454 Pro Thr Asn Leu Ile His Leu Phe Gln Glu Asn Ser Asp Ile Met Asn
      2455          1555              1560              1565
      2457 Ser Leu Ile Glu Ser Trp Cys Gln Asn Ser Glu Val Lys Arg Tyr Leu
      2458      1570              1575              1580
      2460 Asn Gly Glu Arg Gly Ala Ile Ser Tyr Pro Arg Gly Ala Asn Lys Leu
E--> 2461 (585)              1590              1595              1600
      2463 Ile Asp Leu Pro Glu Asp Tyr Ser Ser Leu Ile Asn Gln Ala Ser Asn
      2464               1605              1610              1615
      2466 Phe Ser Cys Pro Lys Ser Gly Gly Asp Lys Ser Arg Ala Pro Thr Leu
      2467          1620              1625              1630
      2469 Cys Leu Val Cys Gly Ser Leu Leu Cys Ser Gln Ser Tyr Cys Cys Gln
      2470          1635              1640              1645
      2472 Ala Glu Leu Glu Gly Glu Asp Val Gly Ala Cys Thr Ala His Thr Tyr
      2473          1650              1655              1660
      2475 Ser Cys Gly Ser Gly Ala Gly Ile Phe Leu Arg Val Arg Glu Cys Gln
```

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```
E--> 2476 (665)              1670             1675                1680
     2478 Val Leu Phe Leu Ala Gly Lys Thr Lys Gly Cys Phe Tyr Ser Pro Pro
     2479                1685             1690               1695
     2481 Tyr Leu Asp Asp Tyr Gly Glu Thr Asp Gln Gly Leu Arg Arg Gly Asn
     2482          1700             1705               1710
     2484 Pro Leu His Leu Cys Gln Glu Arg Phe Arg Lys Ile Gln Lys Leu Trp
     2485       1715             1720             1725
     2487 Gln Gln His Ser Ile Thr Glu Glu Ile Gly His Ala Gln Glu Ala Asn
     2488    1730             1735             1740
     2490 Gln Thr Leu Val Gly Ile Asp Trp Gln His Leu
E--> 2491 (745)             1750             1755
     2955 <210> SEQ ID NO: 18
     2956 <211> LENGTH: 5205
     2957 <212> TYPE: DNA
     2958 <213> ORGANISM: Homo sapiens
     2960 <400> SEQUENCE: 18
     2961 atggcggacg aggaggctgg aggtactgag aggatggaaa tcagcgcgga gttaccccag 60
     2963 accccctcagc gtctggcatc ttggtgggat cagcaagttg attttttatac tgctttcttg 120
     2965 catcatttgg cacaattggt gccagaaatt tactttgctg aaatggaccc agacttggaa 180
     2967 aagcaggagg aaagtgtaca aatgtcaata ttcactccac tggaatggta cttatttgga 240
     2969 gaagatccag atatttgctt agagaaattg aagcacagtg gagcatttca gctttgtggg 300
     2971 agggttttca aaagtggaga gacaacctat tcttgcaggg attgtgcaat tgatccaaca 360
     2973 tgtgtactct gtatggactg cttccaggac agtgttcata aaaatcatcg ttacaagatg 420
     2975 catacttcta ctggaggagg gttctgtgac tgtggagaca cagaggcatg gaaaactggc 480
     2977 cctttttgtg taaatcatga acctggaaga gcaggtacta taaaagagaa ttcacgctgt 540
     2979 ccgttgaatg aagaggtaat tgtccaagcc aggaaaatat ttccttcagt gataaaatat 600
     2981 gtcgtagaaa tgactatatg ggaagaggaa aaagaactgc ctcctgaact ccagataagg 660
E--> 2983 knryycvndh hsydhgtcat atacagccta caaagagctc ttgactgtga gctcgcagag 720
     2985 gcccagttgc ataccactgc cattgacaaa gagggtcgtc gggctgttaa agcgggagct 780
     2987 tatgctgctt gccaggaagc aaaggaagat ataaagagtc attcagaaaa tgtctctcaa 840
     2989 catccacttc atgtagaagt attacactca gagattatgg ctcatcagaa atttgctttg 900
     2991 cgtcttggtt cctggatgaa caaaattatg agctattcaa gtgactttag gcagatcttt 960
     2993 tgccaagcat gccttagaga agaacctgac tcggagaatc cctgtctcat aagcaggtta 1020
     2995 atgctttggg atgcaaagct ttataaaggt gcccgtaaga tccttcatga attgatcttc 1080
     2997 agcagttttt ttatggagat ggaatacaaa aaactctttg ctatggaatt tgtgaagtat 1140
     2999 tataaacaac tgcagaaaga atatatcagt gatgatcatg acagaagtat ctctataact 1200
     3001 gcactttcag ttcagatgtt tactgttcct actctggctc gacatcttat tgaagagcag 1260
     3003 aatgttatct ctgtcattac tgaaactctg ctagaagttt tacctgagta cttggacagg 1320
     3005 aacaataaat tcaacttcca gggttatagc caggacaaat gggaagagt atatgcagta 1380
     3007 atatgtgacc taaagtatat cctgatcagc aaacccacaa tatggacaga aagattaaga 1440
     3009 atgcagttcc ttgaaggttt tcgatctttt ttgaagattc ttacctgtat gcaggggaatg 1500
     3011 gaagaaatcc gaagacaggt tgggcaacac attgaagtgg atcctgattg ggaggctgcc 1560
     3013 attgctatac agatgcaatt gaagaatatt ttactcatgt ccaagagtg gtgtgcttgt 1620
     3015 gatgaagaac tcttacttgt ggcttataaa gaatgtcaca aagctgtgat gaggtgcagt 1680
     3017 accagtttca tatctagtag caagacagta gtacaatcgt gtggacatag tttggaaaca 1740
     3019 aagtcctaca gagtatctga ggatcttgta agcatacatc tgccactctc taggaccctt 1800
     3021 gctggtcttc atgtacgttt aagcaggctg ggtgctgttt caagactgca tgaatttgtg 1860
     3023 tcttttgagg actttcaagt agaggtacta gtggaatatc ctttacgttg tctggtgttg 1920
     3025 gttgcccagg ttgttgctga gatgtggcga agaaatggac tgtctcttat tagccaggtg 1980
```

```
3027 ttttattacc aagatgttaa gtgcagagaa gaaatgtatg ataaagatat catcatgctt 2040
3029 cagattggtg catctttaat ggatcccaat aagttcttgt tactggtact tcagaggtat 2100
3031 gaacttgccg aggcttttaa caagaccata tctacaaaag accaggattt gattaaacaa 2160
3033 tataatacac taatagaaga aatgcttcag gtcctcatct atattgtggg tgagcgttat 2220
3035 gtacctggag tgggaaatgt gaccaaagaa gaggtcacaa tgagagaaat cattcacttg 2280
3037 ctttgcattg aacccatgcc acacagtgcc attgccaaaa atttacctga gaatgaaaat 2340
3039 aatgaaactg gcttagagaa tgtcataaac aaagtggcca catttaagaa accaggtgta 2400
3041 tcaggccatg gagtttatga actaaaagat gaatcactga aagacttcaa tatgtacttt 2460
3043 tatcattact ccaaaaccca gcatagcaag gctgaacata tgcagaagaa aaggagaaaa 2520
3045 caagaaaaca aagatgaagc attgccgcca ccaccacctc ctgaattctg ccctgctttc 2580
3047 agcaaagtga ttaaccttct caactgtgat atcatgatgt acattctcag gaccgtattt 2640
3049 gagcgggcaa tagacacaga ttctaacttg tggaccgaag ggatgctcca aatggctttt 2700
3051 catattctgg cattgggttt actagaagag aagcaacagc ttcaaaaagc tcctgaagaa 2760
3053 gaagtaacat ttgactttta tcataaggct tcaagattgg gaagttcagc catgaatata 2820
3055 caaatgcttt tggaaaaact caaaggaatt ccccagttag aaggccagaa ggacatgata 2880
3057 acgtggatac ttcagatgtt tgacacagtg aagcgattaa gagaaaaatc ttgtttaatt 2940
3059 gtagcaacca catcaggatc ggaatctatt aagaatgatg agattactca tgataaagaa 3000
3061 aaagcagaac gaaaaagaaa agctgaagct gctaggctac atcgccagaa gatcatggct 3060
3063 cagatgtctg ccttacagaa aaacttcatt gaaactcata aactcatgta tgacaataca 3120
3065 tcagaaatgc ctgggaaaga agattccatt atggaggaag agagcacccc agcagtcagt 3180
3067 gactactcta gaattgcttt gggtcctaaa cggggtccat ctgttactga aaaggaggtg 3240
3069 ctgacgtgca tcctttgcca agaagaacag gaggtgaaaa tagaaaataa tgccatggta 3300
3071 ttatcggcct gtgtccagaa atctactgcc ttaacccagc acaggggaaa acccatagaa 3360
3073 ctctcaggag aagccctaga cccactttc atggatccag acttggcata tggaacttat 3420
3075 acaggaagct gtggtcatgt aatgcacgca gtgtgctggc agaagtattt tgaagctgta 3480
3077 cagctgagct ctcagcagcg cattcatgtt gaccttttg acttggaaag tggagaatat 3540
3079 ctttgccctc tttgcaaatc tctgtgcaat actgtgatcc ccattattcc tttgcaacct 3600
3081 caaaagataa acagtgagaa tgcagatgct cttgctcaac ttttgaccct ggcacggtgg 3660
3083 atacagactg ttctggccag aatatcaggt tataatataa gacatgctaa aggagaaaac 3720
3085 ccaattccta ttttctttaa tcaaggaatg ggagattcta ctttggagtt ccattccatc 3780
3087 ctgagttttg gcgttgagtc ttcgattaaa tattcaaata gcatcaagga aatggttatt 3840
3089 ctctttgcca caacaattta tagaattgga ttgaaagtgc cacctgatga aagggatcct 3900
3091 cgagtcccca tgctgacctg gagcacctgc gctttcacta tccaggcaat tgaaaatcta 3960
3093 ttgggagatg aaggaaaacc tctgtttgga gcacttcaaa ataggcagca taatggtctg 4020
3095 aaagcattaa tgcagtttgc agttgcacag aggattacct gtcctcaggt cctgatacag 4080
3097 aaacatctgg ttcgtcttct atcagttgtt cttcctaaca taaaatcaga agatacacca 4140
3099 tgccttctgt ctatagatct gtttcatgtt ttggtgggtg ctgtgttagc attcccatcc 4200
3101 ttgtattggg atgaccctgt tgatctgcag ccttcttcag ttagttcttc ctataaccac 4260
3103 ctttatctct tccatttgat caccatggca cacatgcttc agatactact tacagtagac 4320
3105 acaggcctac cccttgctca ggttcaagaa gacagtgaag aggctcattc cgcatcttct 4380
3107 ttctttgcag aaatttctca atatacaagt ggctccattg ggtgtgatat tcctggctgg 4440
3109 tatttgtggg tctcactgaa gaatggcatc accccttatc ttcgctgtgc tgcattgttt 4500
3111 ttccactatt tacttggggt aactccgcct gaggaactgc ataccaattc tgcagaagga 4560
3113 gagtacagtg cactctgtag ctatctatct ttacctacaa atttgttcct gctcttccag 4620
3115 gaatattggg atactgtaag gcccttgctc cagaggcggt gtgcagatcc tgccttacta 4680
3117 aactgtttga agcaaaaaaa caccgtggtc aggtacccta gaaaaagaaa tagtttgata 4740
3119 gagcttcctg atgactatag ctgcctcctg aatcaagctt ctcatttcag gtgcccacgg 4800
3121 tctgcagatg atgagcgaaa gcatcctgtc ctctgccttt tctgtggggc tatactatgt 4860
3123 tctcagaaca tttgctgcca ggaaattgtg aacggggaag aggttggagc ttgcattttt 4920
```

```
3125 cacgcacttc actgtggagc cggagtctgc attttcctaa aaatcagaga atgccgagtg 4980
3127 gtcctggttg aaggtaaagc cagaggctgt gcctatccag ctccttactt ggatgaatat 5040
3129 ggagaaacag accctggcct gaagaggggc aacccccttc atttatctcg tgagcggtat 5100
3131 cggaagctcc atttggtctg gcaacaacac tgcattatag aagagattgc taggagccaa 5160
3133 gagactaatc agatgttatt tggattcaac tggcagttac tgtga         5205
3136 <210> SEQ ID NO: 19
3137 <211> LENGTH: (1735) 1734 (p.21)
3138 <212> TYPE: PRT
3139 <213> ORGANISM: Homo sapiens
3141 <400> SEQUENCE: 19
3142 Ala Met Glu Gly Asn Met Ala Asp Glu Glu Ala Gly Gly Thr Glu Arg
3143   1               5                  10                  15
3145 Met Glu Ile Ser Ala Glu Leu Pro Gln Thr Pro Gln Arg Leu Ala Ser
3146              20                  25                  30
3148 Trp Trp Asp Gln Gln Val Asp Phe Tyr Thr Ala Phe Leu His His Leu
3149         35                  40                  45
3151 Ala Gln Leu Val Pro Glu Ile Tyr Phe Ala Glu Met Asp Pro Asp Leu
3152      50                  55                  60
3154 Glu Lys Gln Glu Glu Ser Val Gln Met Ser Ile Phe Thr Pro Leu Glu
3155  65                  70                  75                  80
3157 Trp Tyr Leu Phe Gly Glu Asp Pro Asp Ile Cys Leu Glu Lys Leu Lys
3158              85                  90                  95
3160 His Ser Gly Ala Phe Gln Leu Cys Gly Arg Val Phe Lys Ser Gly Glu
3161             100                 105                 110
3163 Thr Thr Tyr Ser Cys Arg Asp Cys Ala Ile Asp Pro Thr Cys Val Leu
3164         115                 120                 125
3166 Cys Met Asp Cys Phe Gln Asp Ser Val His Lys Asn His Arg Tyr Lys
3167     130                 135                 140
3169 Met His Thr Ser Thr Gly Gly Gly Phe Cys Asp Cys Gly Asp Thr Glu
3170 145                 150                 155                 160
3172 Ala Trp Lys Thr Gly Pro Phe Cys Val Asn His Glu Pro Gly Arg Ala
3173              165                 170                 175
3175 Gly Thr Ile Lys Glu Asn Ser Arg Cys Pro Leu Asn Glu Glu Val Ile
3176             180                 185                 190
3178 Val Gln Ala Arg Lys Ile Phe Pro Ser Val Ile Lys Tyr Val Val Glu
3179             195                 200                 205
3181 Met Thr Ile Trp Glu Glu Glu Lys Glu Leu Pro Pro Glu Leu Gln Ile
3182     210                 215                 220
3184 Arg Glu Lys Asn Glu Arg Tyr Tyr Cys Val Leu Phe Asn Asp Glu His
3185 225                 230                 235                 240
3187 His Ser Tyr Asp His Val Ile Tyr Ser Leu Gln Arg Ala Leu Asp Cys
3188             245                 250                 255
3190 Glu Leu Ala Glu Ala Gln Leu His Thr Thr Ala Ile Asp Lys Glu Gly
3191             260                 265                 270
3193 Arg Arg Ala Val Lys Ala Gly Ala Tyr Ala Ala Cys Gln Glu Ala Lys
3194             275                 280                 285
3196 Glu Asp Ile Lys Ser His Ser Glu Asn Val Ser Gln His Pro Leu His
3197     290                 295                 300
3199 Val Glu Val Leu His Ser Glu Ile Met Ala His Gln Lys Phe Ala Leu
```

```
3200 305                      310               315                   320
3202 Arg Leu Gly Ser Trp Met Asn Lys Ile Met Ser Tyr Ser Ser Asp Phe
3203                  325               330                   335
3205 Arg Gln Ile Phe Cys Gln Ala Cys Leu Arg Glu Glu Pro Asp Ser Glu
3206              340               345                   350
3208 Asn Pro Cys Leu Ile Ser Arg Leu Met Leu Trp Asp Ala Lys Leu Tyr
3209          355               360                   365
3211 Lys Gly Ala Arg Lys Ile Leu His Glu Leu Ile Phe Ser Ser Phe Phe
3212      370               375                   380
3214 Met Glu Met Glu Tyr Lys Lys Leu Phe Ala Met Glu Phe Val Lys Tyr
3215 385               390                   395                   400
3217 Tyr Lys Gln Leu Gln Lys Glu Tyr Ile Ser Asp Asp His Asp Arg Ser
3218              405               410                   415
3220 Ile Ser Ile Thr Ala Leu Ser Val Gln Met Phe Thr Val Pro Thr Leu
3221          420               425                   430
3223 Ala Arg His Leu Ile Glu Glu Gln Asn Val Ile Ser Val Ile Thr Glu
3224          435               440                   445
3226 Thr Leu Leu Glu Val Leu Pro Glu Tyr Leu Asp Arg Asn Asn Lys Phe
3227      450               455                   460
3229 Asn Phe Gln Gly Tyr Ser Gln Asp Lys Leu Gly Arg Val Tyr Ala Val
3230 465               470                   475                   480
3232 Ile Cys Asp Leu Lys Tyr Ile Leu Ile Ser Lys Pro Thr Ile Trp Thr
3233              485               490                   495
3235 Glu Arg Leu Arg Met Gln Phe Leu Glu Gly Phe Arg Ser Phe Leu Lys
3236              500               505                   510
3238 Ile Leu Thr Cys Met Gln Gly Met Glu Glu Ile Arg Arg Gln Val Gly
3239          515               520                   525
3241 Gln His Ile Glu Val Asp Pro Asp Trp Glu Ala Ala Ile Ala Ile Gln
3242      530               535                   540
3244 Met Gln Leu Lys Asn Ile Leu Leu Met Phe Gln Glu Trp Cys Ala Cys
3245 545               550               555                   560
3247 Asp Glu Glu Leu Leu Leu Val Ala Tyr Lys Glu Cys His Lys Ala Val
3248              565               570                   575
3250 Met Arg Cys Ser Thr Ser Phe Ile Ser Ser Ser Lys Thr Val Val Gln
3251          580               585                   590
3253 Ser Cys Gly His Ser Leu Glu Thr Lys Ser Tyr Arg Val Ser Glu Asp
3254          595               600                   605
3256 Leu Val Ser Ile His Leu Pro Leu Ser Arg Thr Leu Ala Gly Leu His
3257      610               615                   620
3259 Val Arg Leu Ser Arg Leu Gly Ala Val Ser Arg Leu His Glu Phe Val
3260 625               630               635                   640
3262 Ser Phe Glu Asp Phe Gln Val Glu Val Leu Val Glu Tyr Pro Leu Arg
3263              645               650                   655
3265 Cys Leu Val Leu Val Ala Gln Val Val Ala Glu Met Trp Arg Arg Asn
3266          660               665                   670
3268 Gly Leu Ser Leu Ile Ser Gln Val Phe Tyr Tyr Gln Asp Val Lys Cys
3269          675               680                   685
3271 Arg Glu Glu Met Tyr Asp Lys Asp Ile Ile Met Leu Gln Ile Gly Ala
3272          690               695                   700
```

```
3274 Ser Leu Met Asp Pro Asn Lys Phe Leu Leu Leu Val Leu Gln Arg Tyr
3275 705              710              715              720
3277 Glu Leu Ala Glu Ala Phe Asn Lys Thr Ile Ser Thr Lys Asp Gln Asp
3278              725              730              735
3280 Leu Ile Lys Gln Tyr Asn Thr Leu Ile Glu Glu Met Leu Gln Val Leu
3281          740              745              750
3283 Ile Tyr Ile Val Gly Glu Arg Tyr Val Pro Gly Val Gly Asn Val Thr
3284          755              760              765
3286 Lys Glu Glu Val Thr Met Arg Glu Ile Ile His Leu Leu Cys Ile Glu
3287     770              775              780
3289 Pro Met Pro His Ser Ala Ile Ala Lys Asn Leu Pro Glu Asn Glu Asn
3290 785              790              795              800
3292 Asn Glu Thr Gly Leu Glu Asn Val Ile Asn Lys Val Ala Thr Phe Lys
3293              805              810              815
3295 Lys Pro Gly Val Ser Gly His Gly Val Tyr Glu Leu Lys Asp Glu Ser
3296              820              825              830
3298 Leu Lys Asp Phe Asn Met Tyr Phe Tyr His Tyr Ser Lys Thr Gln His
3299       835              840              845
3301 Ser Lys Ala Glu His Met Gln Lys Lys Arg Arg Lys Gln Glu Asn Lys
3302     850              855              860
3304 Asp Glu Ala Leu Pro Pro Pro Pro Pro Pro Glu Phe Cys Pro Ala Phe
3305 865              870              875              880
3307 Ser Lys Val Ile Asn Leu Leu Asn Cys Asp Ile Met Met Tyr Ile Leu
3308              885              890              895
3310 Arg Thr Val Phe Glu Arg Ala Ile Asp Thr Asp Ser Asn Leu Trp Thr
3311          900              905              910
3313 Glu Gly Met Leu Gln Met Ala Phe His Ile Leu Ala Leu Gly Leu Leu
3314          915              920              925
3316 Glu Glu Lys Gln Gln Leu Gln Lys Ala Pro Glu Glu Glu Val Thr Phe
3317     930              935              940
3319 Asp Phe Tyr His Lys Ala Ser Arg Leu Gly Ser Ser Ala Met Asn Ile
3320 945              950              955              960
3322 Gln Met Leu Leu Glu Lys Leu Lys Gly Ile Pro Gln Leu Glu Gly Gln
3323              965              970              975
3325 Lys Asp Met Ile Thr Trp Ile Leu Gln Met Phe Asp Thr Val Lys Arg
3326          980              985              990
3328 Leu Arg Glu Lys Ser Cys Leu Ile Val Ala Thr Thr Ser Gly Ser Glu
3329          995              1000             1005
3331 Ser Ile Lys Asn Asp Glu Ile Thr His Asp Lys Glu Lys Ala Glu Arg
3332     1010             1015             1020
3334 Lys Arg Lys Ala Glu Ala Ala Arg Leu His Arg Gln Lys Ile Met Ala
3335 1025             1030             1035             1040
3337 Gln Met Ser Ala Leu Gln Lys Asn Phe Ile Glu Thr His Lys Leu Met
3338              1045             1050             1055
3340 Tyr Asp Asn Thr Ser Glu Met Pro Gly Lys Glu Asp Ser Ile Met Glu
3341              1060             1065             1070
3343 Glu Glu Ser Thr Pro Ala Val Ser Asp Tyr Ser Arg Ile Ala Leu Gly
3344          1075             1080             1085
3346 Pro Lys Arg Gly Pro Ser Val Thr Glu Lys Glu Val Leu Thr Cys Ile
```

RAW SEQUENCE LISTING   DATE: 01/27/2004
PATENT APPLICATION: **US/10/758,636**   TIME: 10:59:30

Input Set : **A:\35966C.txt**
Output Set: **N:\CRF4\01272004\J758636.raw**

```
3347    1090                   1095                1100
3349 Leu Cys Gln Glu Glu Gln Glu Val Lys Ile Glu Asn Asn Ala Met Val
3350 1105                1110                1115               1120
3352 Leu Ser Ala Cys Val Gln Lys Ser Thr Ala Leu Thr Gln His Arg Gly
3353              1125                1130                1135
3355 Lys Pro Ile Glu Leu Ser Gly Glu Ala Leu Asp Pro Leu Phe Met Asp
3356              1140               1145                1150
3358 Pro Asp Leu Ala Tyr Gly Thr Tyr Thr Gly Ser Cys Gly His Val Met
3359          1155                1160                1165
3361 His Ala Val Cys Trp Gln Lys Tyr Phe Glu Ala Val Gln Leu Ser Ser
3362     1170                1175                1180
3364 Gln Gln Arg Ile His Val Asp Leu Phe Asp Leu Glu Ser Gly Glu Tyr
3365 1185                1190                1195               1200
3367 Leu Cys Pro Leu Cys Lys Ser Leu Cys Asn Thr Val Ile Pro Ile Ile
3368              1205                1210                1215
3370 Pro Leu Gln Pro Gln Lys Ile Asn Ser Glu Asn Ala Asp Ala Leu Ala
3371              1220                1225                1230
3373 Gln Leu Leu Thr Leu Ala Arg Trp Ile Gln Thr Val Leu Ala Arg Ile
3374          1235                1240          .       1245
3376 Ser Gly Tyr Asn Ile Arg His Ala Lys Gly Glu Asn Pro Ile Pro Ile
3377     1250                1255                1260
3379 Phe Phe Asn Gln Gly Met Gly Asp Ser Thr Leu Glu Phe His Ser Ile
3380 1265                1270                1275               1280
3382 Leu Ser Phe Gly Val Glu Ser Ser Ile Lys Tyr Ser Asn Ser Ile Lys
3383              1285                1290           . 1295
3385 Glu Met Val Ile Leu Phe Ala Thr Thr Ile Tyr Arg Ile Gly Leu Lys
3386          1300                1305                1310
3388 Val Pro Pro Asp Glu Arg Asp Pro Arg Val Pro Met Leu Thr Trp Ser
3389          1315  .             1320                1325
3391 Thr Cys Ala Phe Thr Ile Gln Ala Ile Glu Asn Leu Leu Gly Asp Glu
3392     1330                1335                1340
3394 Gly Lys Pro Leu Phe Gly Ala Leu Gln Asn Arg Gln His Asn Gly Leu
3395 1345                1350                1355               1360
3397 Lys Ala Leu Met Gln Phe Ala Val Ala Gln Arg Ile Thr Cys Pro Gln
3398    -              1365                1370                1375
3400 Val Leu Ile Gln Lys His Leu Val Arg Leu Leu Ser Val Val Leu Pro
3401          1380                1385                1390
3403 Asn Ile Lys Ser Glu Asp Thr Pro Cys Leu Leu Ser Ile Asp Leu Phe
3404          1395                1400                1405  .
3406 His Val Leu Val Gly Ala Val Leu Ala Phe Pro Ser Leu Tyr Trp Asp
3407 -  1410                1415                1420
3409 Asp Pro Val Asp Leu Gln Pro Ser Ser Val Ser Ser Ser Tyr Asn His
3410 1425                1430                1435               1440
3412 Leu Tyr Leu Phe His Leu Ile Thr Met Ala His Met Leu Gln Ile Leu
3413              1445                1450                1455
3415 Leu Thr Val Asp Thr Gly Leu Pro Leu Ala Gln Val Gln Glu Asp Ser
3416          1460                1465                1470
3418 Glu Glu Ala His Ser Ala Ser Ser Phe Phe Ala Glu Ile Ser Gln Tyr
3419          1475                1480                1485
```

RAW SEQUENCE LISTING   DATE: 01/27/2004
PATENT APPLICATION: US/10/758,636   TIME: 10:59:30

Input Set : A:\35966C.txt
Output Set: N:\CRF4\01272004\J758636.raw

```
3421 Thr Ser Gly Ser Ile Gly Cys Asp Ile Pro Gly Trp Tyr Leu Trp Val
3422     1490                1495                1500
3424 Ser Leu Lys Asn Gly Ile Thr Pro Tyr Leu Arg Cys Ala Ala Leu Phe
3425 1505                1510                1515                1520
3427 Phe His Tyr Leu Leu Gly Val Thr Pro Pro Glu Glu Leu His Thr Asn
3428                1525                1530                1535
3430 Ser Ala Glu Gly Glu Tyr Ser Ala Leu Cys Ser Tyr Leu Ser Leu Pro
3431                1540                1545                1550
3433 Thr Asn Leu Phe Leu Leu Phe Gln Glu Tyr Trp Asp Thr Val Arg Pro
3434                1555                1560                1565
3436 Leu Leu Gln Arg Arg Cys Ala Asp Pro Ala Leu Leu Asn Cys Leu Lys
3437     1570                1575                1580
3439 Gln Lys Asn Thr Val Val Arg Tyr Pro Arg Lys Arg Asn Ser Leu Ile
3440 1585                1590                1595                1600
3442 Glu Leu Pro Asp Asp Tyr Ser Cys Leu Leu Asn Gln Ala Ser His Phe
3443                1605                1610                1615
3445 Arg Cys Pro Arg Ser Ala Asp Asp Glu Arg Lys His Pro Val Leu Cys
3446                1620                1625                1630
3448 Leu Phe Cys Gly Ala Ile Leu Cys Ser Gln Asn Ile Cys Cys Gln Glu
3449                1635                1640                1645
3451 Ile Val Asn Gly Glu Glu Val Gly Ala Cys Ile Phe His Ala Leu His
3452     1650                1655                1660
3454 Cys Lys Ala Arg Gly Cys Ala Tyr Pro Ala Pro Tyr Leu Asp Glu Tyr
3455 1665                1670                1675                1680
3457 Gly Glu Thr Asp Pro Gly Leu Lys Arg Gly Asn Pro Leu His Leu Ser
3458                1685                1690                1695
3460 Arg Glu Arg Tyr Arg Lys Leu His Leu Val Trp Gln Gln His Cys Ile
3461                1700                1705                1710
3463 Ile Glu Glu Ile Ala Arg Ser Gln Glu Thr Asn Gln Met Leu Phe Gly
3464     1715                1720                1725
```
E--> 3466 Phe Asn Trp Gln Leu Leu *
E--> 3467   1730

1735 delete

DO NOT include ending stop codon.

VARIABLE LOCATION SUMMARY   DATE: 01/27/2004
PATENT APPLICATION: US/10/758,636   TIME: 10:59:31

Input Set : A:\35966C.txt
Output Set: N:\CRF4\01272004\J758636.raw

error explanation

Use of n's or Xaa's(NEW RULES):
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
in <220> to <223> section, please explain location of n or Xaa, and which
residue n or Xaa represents.

Seq#:18; N Pos. 662,668

```
<210> 16
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: peptide

<400> 16
Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg
 1               5                   10
```

insufficient explanation.
Give source of genetic material.
(see item 11 on Error Summary sheet)

L:11 M:270 C: Current Application Number differs, Replaced Current Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:710 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
M:332 Repeated in SeqNo=2
L:1537 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:4
M:332 Repeated in SeqNo=4
L:2356 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:6
M:332 Repeated in SeqNo=6
L:2983 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:18
L:3466 M:342 E: Invalid Stop Code On Error, STOP CODON:*
L:3467 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:19